

SYR-HDAC-5003-U.ST25  
SEQUENCE LISTING

<110> SYRRX, INC.  
 <120> HISTONE DEACETYLASE INHIBITORS  
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 <140> Not Yet Assigned  
 <141> 2003-10-09  
 <150> 60/419,929  
 <151> 2002-10-21  
 <160> 3  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens  
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 <221> Amino acid sequence for full length human wild type HDAC8  
 <222> (1)..(377)  
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 <308> Genbank Accession Number NP\_060956  
 <309> 2001-02-26  
 <313> (1)..(377)  
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 Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala  
 20 25 30  
 Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr  
 35 40 45  
 Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met  
 50 55 60  
 Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln  
 65 70 75 80  
 Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr  
 85 90 95  
 Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala  
 100 105 110

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Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp  
115 120 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala  
130 135 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu  
145 150 155 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp  
165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr  
180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe  
195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Trp Tyr  
210 215 220

Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr  
225 230 235 240

Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn  
245 250 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp  
260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu  
275 280 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly  
290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly  
305 310 315 320

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe  
325 330 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys  
340 345 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr  
355 360 365

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Ile Lys Gly Asn Leu Lys His Val Val  
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<210> 2  
<211> 1134  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Human cDNA sequence encoding residues 1-377 of HDAC8  
<222> (1)..(1134)  
<223>

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<308> Genbank Accession Number NM\_018486  
<309> 2001-02-26  
<313> (1)..(1134)

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gtgcattctt tgattgaagc atatgactg cataagcaga tgaggatagt taagcctaaa 180  
gtggcctcca tggaggagat ggccaccttc cacactgatg cttatctgca gcatctccag 240  
aaggtcagcc aagagggcga tgatgatcat ccggactcca tagaatatgg gctaggttat 300  
gactgcccag ccactgaagg gatatttgac tatgcagcag ctataggagg ggctacgatac 360  
acagctgccc aatgcctgat tgacggaatg tgcaaagtag caattaactg gtctggaggg 420  
tggcatcatg caaagaaaga tgaagcatct gggtttttgtt atctcaatga tgctgtcctg 480  
ggaatattac gattgcgacg gaaatttgag cgtattctct acgtggattt ggatctgcac 540  
catggagatg gtgtagaaga cgcattcagt ttcacctcca aagtcatgac cgtgtccctg 600  
cacaaattct ccccaggatt tttcccagga acaggtgacg tgtctgatgt tggcctaggg 660  
aagggatggt actacagtgt aaatgtgccc attcaggatg gcatacaaga tgaaaaatat 720  
taccagatct gtgaaagcgt actaaaggaa gtataccaag cctttaatcc caaagcagtg 780  
gtcttacagc tgggagctga cacaatagct ggggatccca tgtgtctcctt taacatgact 840  
ccagtgggaa ttggcaagtg tcttaagtac atccttcaat ggcagttggc aacactcatt 900  
ttgggaggag gaggtataaa ccttgccaac acggctcgat gctggacata cttgaccggg 960  
gtcatcctag ggaaaacact atcctctgag atcccagatc atgagttttt cacagcatat 1020  
ggctctgatt atgtgctgga aatcacgcca agctgccggc cagaccgcaa tgagccccac 1080  
cgaatccaac aaatcctcaa ctacatcaaa gggaatctga agcatgtggt ctatg 1134

<210> 3  
<211> 385  
<212> PRT

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<213> Homo sapiens

<220>

<221> Amino acid sequence for residues 1-377 of HDAC8 with a cleavable N-terminal 6x-histidine tag

<222> (1)..(385)

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<221> Cleavable N-terminal 6x-histidine tag

<222> (1)..(8)

<223>

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Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr  
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met  
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile  
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr  
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp  
85 90 95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala  
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile  
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn  
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe  
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys  
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly  
180 185 190

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Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu  
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp  
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln  
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu  
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu  
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr  
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu  
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala  
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser  
325 330 335

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr  
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His  
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val  
370 375 380

Val  
385